IN THE CLAIMS

Please amend the Claims as follows:

Claims 1-24. (Canceled)

25.   (New) A computer implemented method of searching genetic data or information for a plurality of query sequences in a set of target sequence fragments, allowing for mismatches at up to n sequence positions, comprising:

a) dividing each query sequence of the plurality of query sequences into n+1 query sequence segments and dividing each target fragment of the target sequence fragments into at least n+1 target sequence fragment segments;

b) for each query sequence of the plurality of query sequences, constructing a first query group and a second query group by distributing query sequence segments there between such that at least n query sequence segments are contained in the second query group;

c) constructing from each target fragment a first target group having a same distribution as the first query group; and

d) for each query sequence of the plurality of query sequences, comparing the first query group with each first target group to identify potential matching target fragments.

26.   (New) The computer implemented method of claim 25, wherein steps (b) to (d) are repeated using different distributions of query sequence segments between the first query group and the second query group.

27.   (New) The computer implemented method of claim 26, wherein steps (b) to (d) are repeated using distinct distributions of query sequence segments between the first query group and the second query group

28.   (New) The computer implemented method of claim 25, further comprising, for

each potential matching target fragment of the potential matching target fragments identified in step (d):

(e) constructing a second target group having a same segment distribution as the second query group of the potential matching query sequences; and

(f) comparing the second query group with the second target group to identify a match, allowing for mismatches in up to n sequence positions.

29.   (New) The computer implemented method of claim 28, wherein step (f) is carried out by applying an exclusive OR operation to a binary representation of each of the second query group and the second target group.

30.   (New) The computer implemented method of claim 29, wherein a result of the exclusive OR operation is analyzed using a lookup table.

31.   (New) The computer implemented method of claim 25, further comprising:
for each distinct distribution of query sequence segments, constructing a first query table indexed by possible values of the first query groups, wherein the entries in the first query table provide access to each second query group by using as an index the value of a corresponding first query group.

32.   (New) The computer implemented method of claim 31, further comprising:
for each distinct distribution of query sequence segments, constructing a second query table providing access to each second query group, wherein the entries in the first query table provide references to appropriate entries in the second query table.

33.   (New) The computer implemented method of claim 31, further comprising:

for each first target group constructed in step (c), implementing step (d) by using each first target group to form an index into the first query table.

34.   (New) The computer implemented method of claim 31, wherein, if two distinct distributions of query sequence segments are such that the first query group of a first distribution is the same as the second query group of a second distribution, respective first query tables for each of the two distinct distributions are at least one of constructed and used concurrently.

35.   (New) The computer implemented method of claim 25, wherein target sequence fragments in the set of target sequence fragments comprise overlapping fragments of one or more target sequences.

36.   (New) The computer implemented method of claim 22, wherein each query sequence of the plurality of query sequences and the target sequence fragments comprise biochemical sequence data.

37.   (New) The computer implemented method of claim 36, wherein each query sequence of the plurality of query sequences and the target sequence fragments are binary encoded.

38.   (New) The computer implemented method of claim 25, wherein **n** is at least two.

39.   (New) The computer implemented method of claim 25, wherein each query sequence of the plurality of query sequences and the target sequence fragments are divided into an even number of query sequence segments and target sequence fragment segments, and further wherein the query sequence segments and the target sequence fragment segments are distributed

in equal numbers between the first query group and the second query group and the first target group and a second target group.

40.   (New) The computer implemented method of claim 25, wherein the n+1 query sequence segments are formed from a splitting of each query sequence of the plurality of query sequences.

41.   (New) The computer implemented method of claim 25, wherein the n+1 query sequence segments are formed from a coding or scrambling of each query sequence of the plurality of query sequences.

42.   (New) The computer implemented method of claim 25, further comprising: using a hash function to split each query sequence of the plurality of query sequences and the target sequence fragments into prefixes and suffixes.

43.   (New) The computer implemented method claim 25, further comprising: constructing or computing at least one hash function table.

44.   (New) An apparatus for searching genetic data or information, comprising:
a memory device, wherein the memory device stores information for searching for a plurality of query sequences in a set of target sequence fragments, allowing for mismatches at up to n sequence positions;
a processing device, wherein the processing device constructs a plurality of first query groups and a plurality of second query groups for storage in the memory device, wherein the processing device constructs, for each query sequence of the plurality of query sequences, a first query group and a second query group, by dividing each query sequence of the plurality of query

sequences into n+1 query sequence segments and distributing the query sequence segments between the first query group and the second query group in one or more ways such that at least n query sequence segments are contained in each second query group, and further wherein the processing device constructs a first target group for each target sequence fragment in the set of target sequence fragments, wherein the processing device constructs a plurality of first target groups, and further wherein one or more of the first target groups have query sequence segment distributions corresponding to the first query groups, and further wherein the processing device, for each query sequence of the plurality of query sequences, compares one or more of the first query groups with one or more of the first target groups and identifies potentially matching query sequences and potentially matching target sequence fragments; and

an output device for outputting information regarding the potentially matching query sequences and the potentially matching target sequence fragments.

45.   (New) The apparatus of claim 44, wherein the processing device constructs, for each query sequence of the plurality of query sequences and for each target sequence fragment, respectively, a plurality of first query groups and second query groups having distinct distributions of segments between the first query groups and the second query groups.

46.   (New) The apparatus of claim 44, wherein the processing device constructs, at least for each target sequence fragment identified by the processing device as a potentially matching target sequence fragment of the potentially matching target sequence fragments, one or more second target groups, wherein one or more of the second target groups has a segment distribution corresponding to the second query groups, and further wherein the processing device, for each identified potentially matching query sequence and for each potentially matching target sequence fragment, compares a corresponding second query group and a second target group to identify a match allowing for mismatches in up to n sequence positions.

47.　(New) The apparatus of claim 44, wherein the processing device, for each distinct distribution of a query sequence segment, constructs a first query table indexed by possible values of the first query groups, wherein entries in the first query table provide access to each second query group by using as an index a value of a corresponding first query group.

48.　(New) The apparatus of claim 47, wherein the processing device, for each distinct distribution of a query sequence segment, constructs a second query table, wherein the second query table provides access to each second query group, and further wherein the entries in the first query table provide reference to appropriate entries in the second query table.

49.　(New) The apparatus of claim 44, wherein the processing device forms the n+1 query sequence segments by splitting each query sequence of the plurality of query sequences.

50.　(New) The apparatus of claim 44, wherein the processing device forms the n+1 query sequence segments by coding or scrambling each query sequence of the plurality of query sequences.

51.　(New) The apparatus of claim 44, wherein the processing device uses a hash function to split the plurality of query sequences and the target sequence fragments into prefixes and suffixes.

52.　(New) The apparatus of claim 44, wherein the processing device constructs or computes at least one hash function table.

53.　(New) The apparatus of claim 44, wherein the apparatus is a personal computer or a desk top computer.

54.   (New) A computer program for use in connection with a device for searching genetic data or information and comprising a computer program code for searching for a plurality of query sequences in a set of target sequence fragments, allowing for mismatches at up to n sequence positions, comprising:

a first program module or portion for constructing in a memory associated with the computer, for each query sequence of the plurality of query sequences, a first query group and a second query group by dividing each query sequence of the plurality of query sequences into n+1 query sequence segments and distributing the query sequence segments between the first query group and the second query group in one or more ways such that at least n query sequence segments are contained in each second query group;

a second program module or portion for constructing in the memory, for each target sequence fragment of the set of target sequence fragments, one or more first target groups having target sequence fragment segment distributions corresponding to the first query groups; and

a third program module or portion for comparing, for each query sequence of the plurality of query sequences, one or more first query groups with corresponding one or more first target groups and to output a result identifying potentially matching query sequences and potentially matching target sequence fragments.

55. (New) The computer program of claim 54, wherein the computer program is stored on a removable computer-readable storage medium.

56. (New) The computer program of claim 54, wherein the computer program is loadable over a network connection.